

## SEQUENCE LISTING

## (1) GENERAL INFORMATION

(i) APPLICANT: Hadlaczky, Gyula  
Szalay, Aladar

(ii) TITLE OF THE INVENTION: ARTIFICIAL CHROMOSOMES, USES THEREOF  
AND METHODS FOR PREPARING ARTIFICIAL CHROMOSOMES

(iii) NUMBER OF SEQUENCES: 34

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Heller Ehrman White & McAuliffe  
(B) STREET: 4350 La Jolla Village Drive, 6th Floor  
(C) CITY: San Diego  
(D) STATE: CA  
(E) COUNTRY: USA  
(F) ZIP: 92122

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette  
(B) COMPUTER: IBM Compatible  
(C) OPERATING SYSTEM: DOS  
(D) SOFTWARE: FastSEQ Version 1.5

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:  
(B) FILING DATE:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/835,682  
(B) FILING DATE: 10-APR-1997  
(C) CLASSIFICATION:

(viii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/695,191  
(B) FILING DATE: 07-AUG-1996  
(C) CLASSIFICATION:

(ix) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/682,080  
(B) FILING DATE: 15-JUL-1996  
(C) CLASSIFICATION:

(x) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/629,822  
(B) FILING DATE: 10-APR-1996  
(C) CLASSIFICATION:

(xi) ATTORNEY/AGENT INFORMATION:

(A) NAME: Seidman, Stephanie L  
(B) REGISTRATION NUMBER: 33,779  
(C) REFERENCE/DOCKET NUMBER: 24601-4021

(xii) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 858-450-8403  
(B) TELEFAX: 858-587-5360  
(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1293 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA  
(iii) HYPOTHETICAL: NO  
(iv) ANTISENSE: NO  
(v) FRAGMENT TYPE:  
(vi) ORIGINAL SOURCE:  
(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GAATTCATCA	TTTTTCANGT	CCTCAAGTGG	ATGTTTCTCA	TTTNCACATG	TTTAAAGTTT	60
TCTCGCCATA	TTCCCTGGTC	TACAGTGTGC	ATTTCCTCAT	TTTNCAGGTT	TTNCAGTGAT	120
TTCTGTCATT	TCAAGTCCCT	AAGTGGATGT	TTCTCATTTN	CCATGAAATTT	CAGTTTTCTN	180
GCCATATTCC	ACGTCTCTACA	GNGGACATTT	CTAAATTTNC	CACCTTTTTTC	AGTTTTCTCT	240
GCCATAITTC	ACGTCTCTAAA	ATGTGTATTT	CTCGTITNCC	GTGATTTTCA	GTITTTCTCG	300
CAGATTCCAG	GTCTCTATAAT	GTGCATTTCT	CATTNNAC	GTITTTTCAGT	GATTTCTGTC	360
TTTTTTCAGT	TGGCAAGTGG	GATGTTTCTC	ATTNNCCATG	ATTNNCAGTT	TTCTTGNAAAT	420
ATTCCATGTC	CTACAATGAT	CATTTTAAAT	TTTCCACCTT	TTTCATTTTC	CACGCCATAT	480
TTCAITGTCCT	AAAGTGATATA	TTTCTCCTTT	TCCGCGATTT	TCAGTTTTCT	CGCCATATTC	540
CAGGTCTCTAC	AGTGTGCATT	CCTCATTTTT	CACCTTTTTTC	ACTGATTTTCG	TCATTTTTC	600
AGTGCCTCAAC	TGGATCTTTT	TAATTTTCCTA	TGATTTTCAG	TTATCTTGTC	ATAITTCATG	660
TCCTACAGTG	GACATTTTCA	AAATTTCCAA	CTTTTTCAAT	TTTCTCTGAC	ATATTTGAGC	720
TGCTAAAGTG	GCATTTCTCT	ATTTCCGCTG	ATTTTCAGTT	TTCTCGGCAT	ATTCCAGTCT	780
CTAATAGTGT	TCATTTCTCT	TTTTTCACGT	TTTTTCAGTG	TTTCTGCATT	TTTTCAGTT	840
GTCAAGGGGA	TTTTTCTCAT	TTTTCCATGAG	TGTCAGTTT	CTTGTCTATAT	TCACGTGCTC	900
ACAGTGACAT	TTCTAAATAT	TATACCTTTT	TCAGTTTTC	TCACCATATT	TCAGTGTCTA	960
AAGTATATAT	TTTCTCATTT	CCCTGATTTT	CAGTTTCTCT	GCCATATTCC	AGGTCCCTACA	1020
GTGTGCTATT	CTCATTTTTC	ACGTTTTCCTA	GTAATTTCTT	CATTTTTTAA	GCCCTCAAAAT	1080
GGATGTTTCT	CATTTTCCAT	GATTTTCAGT	TTTCTTGCCA	TACACCATGT	CCTACAGTGG	1140
ACATTTCTAA	ATTATCCACC	TTTTTCAGTT	TTTCTCGCAT	ACATTTTCAG	TTCTAAAGTT	1200
TGTATTTCTA	ATTTTCAGTG	ATTTTCAGTT	TTTCTCGCAT	ATTTCCAGGAC	CTACAGTGTG	1260
CATTTTCTCAT	TTTTTCAGTT	TTTTTCAGTAA	TTT			1293

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1044 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA  
(iii) HYPOTHETICAL: NO  
(iv) ANTISENSE: NO  
(v) FRAGMENT TYPE:  
(vi) ORIGINAL SOURCE:  
(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

AGGCCTATGG	TGAAAAAGGA	AATATCTTCC	CCTGAAAACT	AGACAGAAGG	ATTCTCAGAA	60
TCTTATTTGT	GATGTGCGCC	CCTCAACTAA	CAGTGTGTGA	GCTTTCTTTT	GATAGAGCAG	120
TTTTTGAAACA	CTCTTTTTGT	AAAATCTGCA	AGAGGATATT	TGGATAGCTT	TGAGGATTTT	180
CGTTGGAAC	GGGATTTGCT	TCATATAAAC	CCTAGACAGA	AGCATTTCTA	GAAGCTTCAT	240
TGGGATGTTT	CAGTTGAAGT	CACAGTGTGT	AAACGATCCC	TTTCATAGAG	CAGGTTTGAA	300
ACACTCTTTT	TGTGTATATC	TGGAAGTGG	CATTTCGAGC	GATCTCAGGA	CTGCGGTGAA	360
AAAGGAAAT	TCTTCCAATA	AAAGCTAGAT	AGAGGCAATG	TCAGAAACCT	TTTTTCATGAT	420
GTATCTACTC	AGCTAACAGA	GTTGAACCTT	CTTTTGAGAG	AGCAGTTTTT	AAACACTCTT	480
TTTGTGAAT	CTGCAAGTGG	ATATTTGTCT	AGCTTTGAG	ATTTCGTTGG	GAACCGGAGT	540
TACATATAAA	AAGCAGACAG	CAGCATTCCC	AGAAACTTCT	TGTGTATGTT	TGCATTTCAAG	600
TCACAGAGTT	GAACTATCCC	TTTCATAGAG	CAGGTTTGAA	ACACACTTTT	TGATGTATCT	660
GGATGTGGAC	ATTTCAGGCC	CTTTCAGGCC	TAGGTGAAA	AGGAAATATC	TTCCCTTGAA	720

AACTAGACAG	AAGCATTCTC	AGAAACTTAT	TTGTGATGTG	CGCCCTCAAC	TAAACAGTGT	780
GAAGCTTTCT	TTTGATAGAG	GCAGTTTGA	AACACTCTTT	TGTGGAAATCT	GCAAGTGGAT	840
ATTGTGCTAG	CTTTGAGGAT	TTCTTTGGAA	ACGGGATTAC	ATATAAAAAAG	CAGACAGCAG	900
CATTCGCCAGA	ATCTTGTTTG	TGATGTTTGC	ATTCAAGTCA	CAGAGTGTAA	CATTCCCTTT	960
CAGAGAGCAG	GTTTGAACAC	TCTTTTATA	GTATCTGGAT	GTGGACATTT	GGAGCGCTTT	1020
CAGGGGGGAT	CCTCTAGAAT	TCCT				1044

## (2) INFORMATION FOR SEQ ID NO:3:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2492 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTGCAGCTGG	GGGTCTCCAA	TCAGGCAGGG	GCCCTTACT	ACTCAGATGG	GGTGGCCGAG	60
TAGGGGAAAG	GGGTGCAGGC	TGCATGAGTG	GACACAGCTG	TAGGACTACC	TGGGGCTGT	120
GGATCTATGG	GGGTGGGGAG	AAGCCCACTG	ACAGTGCCTA	GAGAGACAA	GGTGGCTTGA	180
GAGGCTCTGA	GGAACATAGA	GCTGGCCATG	TTGGGGCCAG	GTCTCAAGCA	GGAAGTGAAG	240
AATGGGACAG	GCTTGAGGAT	ACTCTACTCA	GTAGCCAGGA	TCTCAAGAG	GCTTGGGGT	300
TGCTATCTGG	TGGTTCAGC	CCCAAGTTTG	AAGGCCCTGG	GCGAGATGCT	CCCAAGACAT	360
ATTACAATGG	AGGAGAGAG	TTGGGAGACC	TGGAGTCAAC	AAACAAACCC	ATGCCAAGAG	420
AGGACATGAG	TAGGSGTGTC	CAGTCCAGCC	CTCTGACTGA	GCTGCATTTG	TCAAAATCCAA	480
AGGCCCCCTG	CTGCCACTTA	GTGGCTGATG	GCATCCACAT	GACCCCTGGC	CACAGCCGTT	540
TAGSGTCTCT	GTGAAGACCA	AGATCCTTGT	TACATTGAAC	GACTCTTAA	TGAGCAGAGA	600
TTTCCACCTA	TTCGAACAA	TCCATCTCG	AAAAAGCCTG	GCGGATGGCA	GGGTTTAGGG	660
CTAAGGCTAG	GAGTAGGGTG	GGATGAAGAT	TATAGTTTCA	GTAAAGGGTT	TAGGGTTAGG	720
GATCAACGTT	GGTTAGAGTG	TAGGGATACA	GTAGGGTACC	GTTAGGGTTA	GGGTTTAGGG	780
TTAGGGGTTA	GGGTTAGGGT	TAGGGTTAGG	GTTAGGGTTA	GGGTTTAGGG	GTTAGGGTTA	840
GGGTTAGGTT	TTGGGGTGGC	GTATTTTGGT	CTTATACGCT	GTGTTCCACT	GGCAATGAAA	900
AGAATTTCTG	TTTTTCCTCT	AGCAATTGT	CATTTTAA	AGAGTTTAGC	AAITCTAACA	960
GATATAGACC	AGCTGTGCTA	TCTCATGTG	GTTTTCAATT	GTAAACCAAT	TGTGGTTTCA	1020
ATGTGTTTAC	TTGCCATCTG	TAGATCTTCT	TTGCGTGAGG	TGTCTGTTCA	GATGTGTGTG	1080
CATTTTCTGN	NTTTNGGCTG	TTTAACTTAT	TGTTTAGTTT	TAATAATTTT	TTTATATATT	1140
GGAAGCAAA	CTTTCTCAGA	TGTGTAATTT	CAAAATTTT	TTCAATATGA	GGCTTGCTTT	1200
TGTCCTCAAC	AAGGTCCTTC	CAGAGATAAC	GAATATATA	GAATATATA	CTGTCACTTC	1260
TTTTGTGAT	ATCTACCTTT	TGTGTCATTT	GTTAAATTT	ATTACCAAC	CCAAAGGCAG	1320
ATAGGCTTTC	TCTATTGTT	TCTCTAGAA	ATTTGTATAG	TTTTGATTT	TTAGTGTAA	1380
GATGATTTTG	AGTGATTAAT	TGTGTAAGTT	GTAAGGTTT	CGTCTATATC	CATATCATTT	1440
CTTATGGTTT	CCAATTAATC	GTCCCTCAC	TATTTTGGG	AAAGACACAG	GATAGTGGGC	1500
TTTGTAGAG	TAGATAGGTA	GCTAGACATG	AACAGGAGGG	GGCCTCCTGG	AAAAGGGAAA	1560
GTCTCCGAAG	GCTCACTTGG	AGGACCCACA	AAAATTCATA	TATTAGTACA	ATCTCTAGTG	1620
CTGGAGTGGA	TGGGCACCTG	TCAATTGTGG	GTAGGAGGGA	AAAGAGGTCC	TATGCAGAAA	1680
GAAACTCCCT	AGAACTCCTC	TGAAGATGCC	CCAATCAITC	ACTCTGCAAT	GATGCTGTTCA	1740
GAATATTGCT	AGCTACATGC	TGATAAGGNN	AAAGGGGACA	TTCTTAAGTG	AAACCTGGCA	1800
CCATAAGTAC	AGATTAGGGC	AGAGAAGGAC	ATTCAAAAGA	GCAAGGCACG	GATAGTACAA	1860
ACGCTGATCG	TGTCAGTTGT	CCTGGGATGG	CGGGAAGGAG	GCTGTGGCCA	GAGTGATTT	1920
GTAATTGATCA	CACACATATG	ACCTCAACCA	ACAGTGAGGA	GTCCTCAAGT	GCTCAAGTGG	1980
GGCAAGATTGG	GGAGCTAAGG	CAGTAGCAGG	AAAACAGCAG	AAAGAAAACA	GGTGAGAGAT	2040
TGAGACAGAG	CAGGAAATGT	GAAAGAAATC	AAAATAAAAT	TCCCTGTGCA	GGACTCTTAG	2100
CGCTGTTAAT	GCATCGCTCA	GTCCTCACTC	TCCCTATTTT	TCTACAAATA	ACTCTTTTCA	2160
CTGTGTTTCT	TTTCAATGAA	TTTATCTGCC	ATCTTTGTAT	TGCTCTTGGT	TGAAAATGTT	2220
TTCTCCAAGT	TAAACAGAA	CTGGGACATC	AGCTCTCCCC	AGTAATAGCT	CGGTTTCAAT	2280
TTGAATTTAC	AGAACTGATG	GGCTTAATAA	CTGGCGCTCT	GACTTTTAGT	GTGACGAGGG	2340

CCGTCACACC	GGGACCAAGA	GTGCCCTGCC	TAGTCCCAT	CTGCCCGCAG	GTGGCGGCTG	2400
CCTCGACACT	GACAGCAATA	GGGTCCGGCA	GTGTCCCAG	CTGCCAGCAG	GGGGCGTACG	2460
ACGACTACAC	TGTGAGCAAG	AGGGCCCTGC	AG			2492

## (2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 28 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GGGGAATTCA TTGGGATGTT TCAGTTGA

28

## (2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CGAAAGTCCC CCCTAGGAGA TCTTAAGGA

29

## (2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 47 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: RNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CCGCTTAATA CTCTGATGAG TCCGTGAGGA CGAAACGCTC TCGCACC

## (2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 25 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CGATTTAAT TAATTAAGCC CGGGC

25

## (2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TAAATTAAAT TAATTCGGC CCGTCGA

27

## (2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 69 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (D) OTHER INFORMATION IL-2 signal sequence
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATG TAC AGG ATG CAA CTC CTG TCT TGC ATT GCA CTA AGT CTT GCA CTT  
 Met Tyr Arg Met Gln Leu Leu Ser Cys Ile Ala Leu Ser Leu Ala Leu

48

GTC ACA AAC AGT GCA CCT ACT  
 Val Thr Asn Ser Ala Pro Thr

69

## (2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 945 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 1...942

(D) OTHER INFORMATION: Renilla Reinformis Luciferase

(x) PUBLICATION INFORMATION:

PATENT NO.: 5,418,155

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

AGC	TTA	AAG	ATG	ACT	TCG	AAA	GTT	TAT	GAT	CCA	GAA	CAA	AGG	AAA	CGG	48
Ser	Leu	Lys	Met	Thr	Ser	Lys	Val	Tyr	Asp	Pro	Glu	Gln	Arg	Lys	Arg	
1				5					10					15		
ATG	ATA	ACT	GGT	CCG	CAG	TGG	TGG	GCC	AGA	TGT	AAA	CAA	ATG	AAT	GTT	96
Met	Ile	Thr	Gly	Pro	Gln	Trp	Trp	Ala	Arg	Cys	Lys	Gln	Met	Asn	Val	
			20					25					30			
CTT	GAT	TCA	TTT	ATT	AAT	TAT	TAT	GAT	TCA	GAA	AAA	CAT	GCA	GAA	AAT	144
Leu	Asp	Ser	Phe	Ile	Asn	Tyr	Tyr	Asp	Ser	Glu	Lys	His	Ala	Glu	Asn	
			35				40					45				
GCT	GTT	ATT	TTT	TTA	CAT	GGT	AAC	GCG	GCC	TCT	TAT	TAT	TTA	TGG	CGA	192
Ala	Val	Ile	Phe	Leu	His	Gly	Asn	Ala	Ala	Ser	Ser	Tyr	Leu	Trp	Arg	
			50			55					60					
CAT	GTT	GTG	CCA	CAT	ATT	GAG	CCA	GTA	GCG	CGG	TGT	ATT	ATA	CCA	GAT	240
His	Val	Val	Pro	His	Ile	Glu	Pro	Val	Ala	Arg	Cys	Ile	Ile	Pro	Asp	
			65			70				75				80		
CTT	ATT	GGT	ATG	GGC	AAA	TCA	GGC	AAA	TCT	GGT	AAT	GGT	TCT	TAT	AGG	288
Leu	Ile	Gly	Met	Gly	Lys	Ser	Gly	Lys	Ser	Gly	Asn	Gly	Ser	Tyr	Arg	
				85					90				95			
TTA	CTT	GAT	CAT	TAC	AAA	TAT	CTT	ACT	GCA	TGG	TTG	AAC	TTC	TTA	ATT	336
Leu	Leu	Asp	His	Tyr	Lys	Tyr	Leu	Thr	Ala	Trp	Leu	Asn	Phe	Leu	Ile	
				100				105					110			
TAC	CAA	AGA	AGA	TCA	TTT	TTT	GTC	GGC	CAT	GAT	TGG	GGT	GCT	TGT	TTG	384
Tyr	Gln	Arg	Arg	Ser	Phe	Phe	Val	Gly	His	Asp	Trp	Gly	Ala	Cys	Leu	
			115				120					125				
GCA	TTT	CAT	TAT	AGC	TAT	GAG	CAT	CAA	GAT	AAG	ATC	AAA	GCA	ATA	GTT	432
Ala	Phe	His	Tyr	Ser	Tyr	Glu	His	Gln	Asp	Lys	Ile	Lys	Ala	Ile	Val	
			130			135					140					
CAC	GCT	GAA	AGT	GTA	GTA	GAT	GTG	ATT	GAA	TCA	TGG	GAT	GAA	TGG	CCT	480
His	Ala	Glu	Ser	Val	Val	Asp	Val	Ile	Glu	Ser	Trp	Asp	Glu	Trp	Pro	
			145			150				155				160		
GAT	ATT	GAA	GAA	GAT	ATT	GCG	TTG	ATC	AAA	TCT	GAA	GAA	GGA	GAA	AAA	528
Asp	Ile	Glu	Glu	Asp	Ile	Ala	Leu	Ile	Lys	Ser	Glu	Glu	Gly	Glu	Lys	
				165				170					175			
ATG	GTT	TTG	GAG	AAT	AAC	TTC	TTC	GTG	GAA	ACC	ATG	TTG	CCA	TCA	AAA	576
Met	Val	Leu	Glu	Asn	Asn	Phe	Phe	Val	Glu	Thr	Met	Leu	Pro	Ser	Lys	
				180				185					190			
ATC	ATG	AGA	AAG	TTA	GAA	CCA	GAA	GAA	TTT	GCA	GCA	TAT	CTT	GAA	CCA	624

Ile Met Arg Lys Leu Glu Pro Glu Glu Phe Ala Ala Tyr Leu Glu Pro  
 195 200 205

TTC AAA GAG AAA GGT GAA GTT CGT CGT CCA ACA TTA TCA TGG CCT CGT 672  
 Phe Lys Glu Lys Gly Glu Val Arg Arg Pro Thr Leu Ser Trp Pro Arg  
 210 215 220

GAA ATC CCG TTA GTA AAA GGT GGT AAA CCT GAC GTT GTA CAA ATT GTT 720  
 Glu Ile Pro Leu Val Lys Gly Gly Lys Pro Asp Val Val Gln Ile Val  
 225 230 235

AGG AAT TAT AAT GCT TAT CTA CGT GCA AGT GAT GAT TTA CCA AAA ATG 768  
 Arg Asn Tyr Asn Ala Tyr Leu Arg Ala Ser Asp Asp Leu Pro Lys Met  
 245 250 255

TTT ATT GAA TCG GAT CCA GGA TTC TTT TCC AAT GCT ATT GTT GAA GGC 816  
 Phe Ile Glu Ser Asp Pro Gly Phe Phe Ser Asn Ala Ile Val Glu Gly  
 260 265 270

GCC AAG AAG TTT CCT AAT ACT GAA TTT GTC AAA GTA AAA GGT CTT CAT 864  
 Ala Lys Lys Phe Pro Asn Thr Glu Phe Val Lys Val Lys Gly Leu His  
 275 280 285

TTT TCG CAA GAA GAT GCA CCT GAT GAA ATG GGA AAA TAT ATC AAA TCG 912  
 Phe Ser Gln Glu Asp Ala Pro Asp Glu Met Gly Lys Tyr Ile Lys Ser  
 290 295 300

TTC GTT GAG CGA GTT CTC AAA AAT GAA CAA TAA 945  
 Phe Val Glu Arg Val Leu Lys Asn Glu Gln  
 305 310

## (2) INFORMATION FOR SEQ ID NO:11:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (iii) HYPOTHETICAL: NO

## (iv) ANTISENSE: NO

## (v) FRAGMENT TYPE:

## (vi) ORIGINAL SOURCE:

## (ix) FEATURE:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TTTGAATTC A TGTACAGGAT GCAACTCTG

30

## (2) INFORMATION FOR SEQ ID NO:12:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (iii) HYPOTHETICAL: NO

## (iv) ANTISENSE: NO

## (v) FRAGMENT TYPE:

## (vi) ORIGINAL SOURCE:

## (ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TTTGAATTC A GTAGGTGCAC TGTTTGTAC

30

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1434 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CCTCCACGCA	CGTTGTGATA	TGTAGATGAT	AATCATTATC	AGAGCAGCGT	TGGGGGATAA	60
TGTCGACATT	TCCACTCCCA	ATGACGGTGA	TGTATAATGC	TCAAGTATTTC	TCCTGCTTTT	120
TTACCACTAA	CTAGGAACTG	GGTTTGGCCT	TAATTCAGAC	AGCCTTGGCT	CTGTCTGGAC	180
AGGTCAGAC	GACTGACACC	ATTAACTCTT	TGTCAGCCTC	AGTGACTACA	GTCTAGATG	240
AACAGGCCTC	AGCTAATGTC	AAGATACAGA	GAGGTCTCAT	GCTGGTTAAT	CACTCATAG	300
ATCTTGTCCA	GATACAACTA	GATGIATTAT	GACAAATAAC	TCAGCAGGSA	TGTGACAAA	360
AGTTTCCGGG	ATTGTGTGTT	ATTTCATTTC	AGTATGTTAA	ATTTACTAGG	ACAGCTAATT	420
TGTCAAAAGG	TCTTTTTCAG	TATATGTTAC	AGAAATGGAT	GGCTGAATTT	GAACAGATCC	480
TTGCGGAATT	GAGACTCTCAG	GTCAACTCCA	CCTGCTTGA	CCTGTGCTG	ACCAAGGAT	540
TACCCAATTG	GATCTCTCTA	CCTCTTCTCT	TCCTTAAAAA	ATGGGTGGGA	TTAATATPAT	600
TGGGAGATAC	ACTTTGCTGT	GGATTAGTGT	TGCTTCTTTG	ATTGTCTCTG	AAGCTTAAGG	660
CCCAACTAG	GAGAGACAG	GGGTATTATG	CCCAGGCGCT	TGCAGGACTA	GAACATGGAG	720
CTTCCCTGA	TATATGCTTA	TCTATGCTTA	GGCAATAGGT	CGCTGGCCAC	TCAGCTCTTA	780
TATCCACAGA	GGCTAGTCTC	ATTGTACGGG	ATAGAGTAG	TGTGCTTCAG	CAGCCCGAGA	840
GAGTTCACAG	GCTAAGCACT	GCAATGGAAA	GGCTCTGCGG	CATATATGTT	CTTATCTTAG	900
GGGACATGTT	CATCTTTTAT	GAAAGTTTCT	TGCTCTAGTT	CCCTTCCCCC	AGGCAAAACG	960
ACACGGGAGC	AGGTACGGGT	TGCTCTGGGT	AAAAGCCTGT	GAGCCTGGGA	GCTAATCTGT	1020
TACATGGCTC	CTTTACCTAC	ACACTGGGGA	TTTGACCTCT	ATCTCCACTC	TCATTAAATAT	1080
GGTGGGCTTA	TTTGTCTCTTA	TTAAAAGGAA	AGGGGGAGAT	GGTGGGAGCC	GGCGCCACAT	1140
TCGCGTTTAT	AAGATGGGCG	TGACAGCTGT	GTTCTAAGTG	GTAACAAAT	AATCTGCGCA	1200
TGTGCCGAGG	GGGTTTCTTC	ACTCCATGTT	CTCTGCTTTC	CCGCTGACGT	CAACTCGGCC	1260
GATGGGCTGC	AGCCAATCAG	GGAGTGACAC	GTCTAGGCG	AAGGAGAATT	CTCCTTAATA	1320
GGGACGGGGT	TTCTGTTCTT	CTCTCTCTCT	TGCTTCTCTC	TCTTGTCTTT	TGCTCTCTTT	1380
GCTTCCCGTA	AAGTGATAAT	GATTATCATC	TACATATCAC	AACGTGCGTG	GAGG	1434

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CCTCCACGCA	CGTTGTGATA	TGTAGATGAT	AATCATTATC	AGAGCAGCGT	TGGGGGATAA	60
TGTCGACATT	TCCACTCCCA	ATGACGGTGA	TGTATAATGC	TCAAGTATTTC	TCCTGCTTTT	120
TTACCACTAA	CTAGGAACTG	GGTTTGGCCT	TAATTCAGAC	AGCCTTGGCT	CTGTCTGGAC	180
AGGTCAGAC	ACAACTAGAT	GTATTATGAC	AAATAACTCA	GCAGGGATGT	GAACAAAAGT	240



TTCCGGGATT	GGGTGTTATT	TCCATCCAGT	ATGTTAAATT	TACTAGGGCA	GCTAATTTGT	300
CAAAAAGTCT	TTTCCAGTAT	ATGTTACAGA	ATTGGATGGC	TGAATTTGAA	CAGATCCCTC	360
GGGAATTGAG	ACTTCAGGTC	AACCTCCAGC	GCTTGGACCT	GTCCTTGACC	AAAGGATTAC	420
CCAATTGGAT	CTCCTCAGCA	TTTTCTTTCT	TTAAAAAATG	GGTGGGATTA	ATATTATTGT	480
GAGATACACT	TGCTGTGGGA	TTAGTGTGTC	TTCTTTGATT	GCTCTGTAAG	CTTAAGGCCCT	540
AAACTAGGAG	GAGCAAGGTG	GTTATTGCC	AGGCGCTTGC	AGGACTAGAA	CATGGAGCTT	600
CCCTCTGATAT	ATCTATGCTT	AGGCAATAGG	TGCTGGGCCA	CTCAGCTCTT	ATATCCCATG	660
AGGCTAGTCT	CATTGACGCG	GATAGAGTGA	GTGTGCTTCA	CGAGCCCGAG	AGAGTTGCAC	720
GGCTAAGCAC	TGCAATGGAA	AGGCTCTGCG	GCATATATGA	GCCTATTCTA	GGGAGACATG	780
TCATCTTTCA	AGAAGGTTGA	GTGTCCAAGT	GTCCTTCCTC	CAGGCAAAAC	GACACGGGAG	840
CAGGTCAGGG	TTGCTCTGGG	TAAAGCCCTG	TGAGCCTAAG	AGCTAATCCT	GTACATGGCT	900
CCTTTACCTA	CACACTGGGG	ATTTGACCTC	TATCTCCACT	CTCATTAATA	TGGGTGGCCT	960
ATTTGCTCTT	ATTTAAAGGA	AAGGGGGAGA	TGTTGGGAGC	CGCGCCCAAC	TTCCCGCTTA	1020
CAAGATGGCG	CTGACAGCTG	TGTTCTAAGT	GGTAAACAAA	TAATCTGCGC	ATGCGCCGAG	1080
GGTGGTCTCT	CACCTCATGT	GCTCTGCCTT	CCCCGTGACG	TCAACTCGGC	CGATGGGCTG	1140
CAGTCAATCA	GGGAGTGACA	CGTCTTAGGC	GAAGGAAAT	TCTCCTTAAT	AGGGACGGGG	1200
TTTCTTTTTC	TCTCTCTCTT	GCTTCTGCTT	CTCTTGCTTC	TTGCTCTCTT	TTCTTGAGAA	1260
TGTAAGAATA	AAGCTTTGCC	GCAGAAGATT	CTGGTCTGTG	GTGTTCTCTC	TGGCCGGCTG	1320
TGAGAACGCG	TCTAATAACA	ATTTGTCGCC	AAACCCGGGT	GATAATGATT	ATCATCTACA	1380
TATCACAAAG	TGCGTGAGAG					1400

## (2) INFORMATION FOR SEQ ID NO:15:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1369 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (iii) HYPOTHETICAL: NO

## (iv) ANTISENSE: NO

## (v) FRAGMENT TYPE:

## (vi) ORIGINAL SOURCE:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CCTCCACGCA	CGTTGTGATA	TGTAGATGAT	AATCAATTATC	ACTTTACGGG	TCCTTTCACT	60
ACAACTGCCA	AGAGGCCGCT	TGCTCTGGTA	ATAGATCTTT	GCTGAAAAGG	CACACACATG	120
ACACATATCT	CAAGGTGGGC	TCATCTGAGC	TGCAGATTCA	GCTTAATATG	AACTCTGCCA	180
ATTGTGTGAA	ATCATAAATG	TTCAAAGTGA	CACCTATTGC	CAGACACAGG	TGCCACCTTT	240
TGGCAATAATA	AACAAACACA	AATTATCTAT	TATATAAAGG	GTGTTAGAAG	ATGCTTTAGA	300
ATACAAATAA	ATCATGGTAG	ATAACAGTAA	GTGAGAGCT	TAAATTTAAT	AAAGTGATAT	360
ACCTAATAAA	AATTAAATTA	AGAAGGTGTG	AATATACTAC	AGTAGGTAA	TTATTTTCAT	420
AAITTAITTTT	CTTTCTTAAT	CCTTTATAAT	GTTTTCTGCT	ATTGTCAATT	GCACATTCAT	480
ATGTTCAATT	CTTCACTGTA	ATGAAGAAAT	GTAGTAAATA	TACTTTCCGA	ACAAGTTGTA	540
TCAAATATGT	TACACTTGTAT	TCCGTGTGTT	ACTTATCATT	TTATATTAT	TTGATTGCA	600
TTCTTCTGTT	ACTTGATATT	ATTACAAGGT	ACATATTAT	TCTCTCAGAT	CTTCATTATA	660
CTCTAACAT	TTTATAACAT	ACTTTATTTA	TTCAATTTCT	ATGTGTGCTG	TGAGGCACAA	720
ATGCCAGAGA	GAACTTGAGC	AGATAAGAGG	ACAAATTGCA	AGAGTCAGTT	ACCTCTCGCT	780
GTTCCTTGGA	AACCTCAGAT	CAAAATCAGG	TGTGACGGCT	TGGCAGCATG	CACCTTTTAC	840
CAGTGCCTCT	ATCTTGCTAG	CCCTGAACAT	CAAGCTTTGC	AGACAGACAG	GCTACACTAA	900
GTGAACCTGG	CATTACAGC	ATGCTATGGT	ATTTATTGTT	ACTTTCTATT	CCATGCCCTT	960
ACTATTCTCA	CTAGTGCTA	GCTAGTACTG	TATTTCCGAG	TAGAAGTTAC	TGAAGAGAAA	1020
TTACTATTGT	TTCTATAGAT	CCTTGATACT	TTCTCAGCAG	ATATAGAGTT	TTAATCAGGT	1080
CTCAGACCTT	TTCTTCACTC	TTATTAAATA	CTAAGTACAA	ATTAAGTTTA	TCCAAAACAG	1140
TACGAGATGT	GATTTTGTGC	AGTTCTACTA	TGATAATAGT	CTAGCTCAT	AAATCTGACA	1200
CACCTATTGC	GAATGTTTTT	GTTAATAAAA	GATTCAGGTG	TTACTCTAGG	TCAAGAGAAAT	1260
ATTAAACATG	AGTCCCAAT	TACAAACTTC	AATAAAGAT	TTGACTCTCC	AGTGGTGSCA	1320
ATATAAAGTG	ATAATGATTA	TCACTCATAT	ATCACACGCT	GCGTGGAGG		1369

## (2) INFORMATION FOR SEQ ID NO:16:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22118 base pairs

- (B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Genomic DNA  
(iii) HYPOTHETICAL: NO  
(iv) ANTISENSE: NO  
(v) FRAGMENT TYPE:  
(vi) ORIGINAL SOURCE:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

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GAATTCGCCCT ATCCCTAATC CAGATTGGTG GAATAACTTG GTATAGATGT TTGTGCATTAA 60
AAAACCCCTGT AGGATCTTCA CTCTAGTGCA CTGTTCAGCA CTGGAAACCTG AATTGTGGGCC 120
CTGAGTGATA GGTCTCTGGGA CATATGCACT TCTGCACAGA CAGACAGACGA GACAGACAGACA 180
CAGACAGACA CAGACAGCGTT ACAACAAAC ACGTTGAGCC GTGTGCCAAC ACACACACAAA 240
ACACCACCTCT GCCCATAAAT ATTGAGGACG TTGATTATT ATTCTGTGTT TGTGAGTCTG 300
TCTGTCTGTC TGCTGTGCTG TCTGTCTGTC TATCAAAACA AAAGAAACCA ACAAAATTATG 360
CCTGCCTGCC TGCCCTGCTGC CTTACACAGA GAAATGATT CTTCAAATCAA TCTAAACAGCA 420
CTCTCAATGT TTGCCCTTTT TCTCTTTCT TAICTTTTTC TTTTCTTTCT CTCTCTTCTT 480
TCTCTCTCTT CTCTCTTCTT TCTCTCTCTT CTCTCTCTCT CTCTCTCTCT CTCTCTCTCT 540
TTCTTTCTCT CTTCATTATTA TCTTTTCTAT ACATAGTTTC CTGTAGAGG TTTTCTCAATG 600
TGCTTTGAAG ACACATTGTGA GGCCTCAATC CTGTAGAGG CTTCCTCTGA TTTTCTAGAA 660
CTGGCATGAA TTGTTGACTC CACTATGACC AGCTTAGTCT TCAAGTCTGA GTTCTAGGAA 720
AGGAGTCTCCA AGAGAGCTGG TTATATTTT CAITTTATAT TGCATTTTAA TTAATAATTAA 780
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AAAGTAGGAG AAAAAGCTGAT GCGTCTCTGT GCATGCTCGA GCGCTCTGA GGGAGCGCTCG 900
TCACCATCTC CACTCTGCA ACACCGGCCG TAGAACCCGG TGAAGGGAGA ACCCAAAGCG 960
ACCTGGAAAC ATAGTCTCAC ATGAAGGCCA GCCACCTTCA TCTGTGTGTT CGGGAGTTCA 1020
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CAGAGAAACG ACATCTTGAA AAAACAAAAA AAATAAATTA AATAAATATA ATTTAAAAAT 1200
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GGGAGGATTT CTGAGTTTGA GCGCAGCCTG GTCTGCAAGT TGAGTTCACG GACAGTCAGG 1320
GCTATACAGA GAAACCCCTG CTGAAAACT AAATAAATTA AAATAAATTA AACTAAAAA 1380
AATATAAATG AAAAATTTTA AAGATTTTGA AAAAATCTAC GAAATCAAC ATACGCCAC 1440
GAGATGGCAA GTAACCTGCAA TCATAGCAGA AATATTATAC ACACACACAC CAGACACTC 1500
TGTCATAAAA TCCAATGTGC CTTTATGATG ATCAAAATTC GATAGTCAGT AATACATGAA 1560
GAATCATATG TCTGAAATAA AAAGCCAGAA CCTTTTCTGC TTTTGTTTTC TTTTGCCTCA 1620
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CTGCCCTGCT GCCTGCCCTCA CTTCTCTGTC CACCCACAGA ACCGAGTCGA ACCTAGGATC 1800
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TCTTCTTTCT TCTTCTTTCT ATTAGTTTTC AATGTAAGTG TGTGTTTGTG TCTATCTCTG 1920
TGCTTATAGG CTGCTGTGCC AGGAGAGGGC AACAGAACTC AGGAGAAACC ACCATCGACG 1980
TCTCTGAGAT AAGTGAAAAA ACAACAAAAA AAGGAAATTC TAATCACATA GAATGTAGAT 2040
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AAAGCATGTG GCCACCACTG CCGCGACTGA TTTCTTCTTT TTTTTTTTTT TGGAAAAATG 2280
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CTGTGCTTAA CTGTGCGCTG TCCCTCACCC CGCTGATTG CCAGCGACGT ACTTTGACTT 3180

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CAAGAACGAT	TTTGCCGTGT	TTACCCGCTC	CCTGTCATAC	TTTCGTTTTT	GGGTGCCCGA	3240
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AGTGGTGGGT	GGGTACGCTG	CTCCGTCGTG	CGTGCCTGAG	TGCCGGAACC	TGAGCTCGGG	3360
AGACCCCTCC	GAGAGACAGA	ATGAGTGAGT	GAATGTGGCG	CGCGCTGACG	GATCTGTATT	3420
GGTTTGTATG	GTGTACCGAG	ACCAATTGCTC	GGCGACACCT	AGTGGTGACA	AGTTTCGGGA	3480
ACGCTCCAGG	CCTCTCAGGT	TGGTGACACA	GGAGAGGGAA	GTGCGTGTGG	TGAGGCGACC	3540
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AGACGCTCTC	AACAAGAGAG	TCGTACAGGG	AGATGGCCAA	AGCAGACCGA	GTTCGCTGTAC	3660
CGCCCTTTTG	GAATAATGCT	AGGGTTGGTG	GCAACGTTAC	TAGGTCGACC	AGAAGGCTTA	3720
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TCCTGTCCCC	TCACCGGGGG	GCACCGTGAC	TCGTAGGCCG	AGAGGACACG	ATGCGCCTGT	4620
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## (2) INFORMATION FOR SEQ ID NO:17:

- (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 42999 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA  
 (iii) HYPOTHETICAL: NO  
 (iv) ANTISENSE: NO  
 (v) FRAGMENT TYPE:  
 (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GCTGACACGC	TGTCCTCTGG	CGACCTGTCTG	TCCGAGAGGT	TGGGCTCCGC	GATGCGCGCG	60
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 CTGGGGTGTG TCCGTAAAGAA CGGCTCTGGG CTGTCTGTGA CATAAACTAG GACGAGGTCC 35040  
 AAGTGTGTTG TCGCAACACT TGGACAGGCA GTTGCTAAAG CTCTCTAGAG AGGTGAATAT 35100  
 AAATGTTTTG TCAGAGCTCT GCTTTTCCCC CTTATTTTAC ATCATGATTG AAAGGGACAT 35160  
 CAGAGGAAAG GATTTCAACG AAGGCTCTTT TGCTCACTT CTGATCCTTT GGTAAAGCCGA 35220  
 TCTGTCTTGG AATATACATG TCCCGACGAT TCCGACGATG TCGCAAGCAG GCATTGTGAT 35280  
 TCAGGAACGA TAATATCATC TTGGCTTTTC TGCTTATGAA ACACCTCCAC GTTAAGAGTAT 35340  
 TGATCCCCCT CTGCAAGCTT GCTGAGATCA ACACAACTAT TCGCAAGCAG GCATTGTGAT 35400  
 TCGCGGTAGT TACAACGTGT ATCTCGGTAG ATCTCGGTAG AGTCTATATG TTATATAGGC CTCTCTGAG 35460  
 CGGTAAGAAC AGGTGCGCAG TAAGAAACAAG GCTTCTCTGT AGTGTACTTC TGCATAAAGG 35520  
 CGTTTCTGGG TCGCTGCGG ATCTCGGTAG CACCGCCATC CTCGAGGCTC AGGCCACTT TCGATATAGA 35580  
 GCGTGGACGG TCCCTCGCAG CACCGCCATC CTCGAGGCTC AGGCCACTT TCGTCAAGTC 35640  
 CACAGGACGG CCCCCCCCCC CATAGCGGCT CGGCGCCGCG CAGCCCTGCT TCTTTTAAAG 35700  
 GCACAGCCGG CGGTATCCGG GGGATGGGGG AGTCCGAGAC AGAATGACTT CTTTATCTGT 35760  
 CTGACTCTGG AAAGCCCGCG CCGTTGTGAT CATTGTCAAA CGGAGATGCA CTCTGTGTT 35820  
 AGAACACCGA TCCACTCCCA AGTTTCAGTG GGGGATGTGA GGGGTGTGGC AGGTAGGACG 35880  
 AAGGACTCTG TCTTCTCTGA TTGCGTCTGC ACAGTGGGGC CTAGGGCTGC AGCTCTCTCC 35940  
 GTGGGACCG CTGACTCCCT CTACCTTTGGG TTCCCTCGCG CACACCTGGG AACCGCGGCG 36000  
 CTGGGACAGT TCTGCGCCTT CTGCGCCTT CAGTGCCTGT CGGAGAACCC ATCTCATGTG 36060  
 CGATGCCCCG GAATCTGTGT GCTCTGCGAA CATTGGAAT CTCTCTCTCTA 36120  
 CGCGCGGACA CCTGAACCA CAGGAGCTCG GACGACACTG GCTTTCTGGG GAGAATGCTG 36180  
 AGAGTCTCTC GCGACTCTC TCTGACTTG AGTCTCTGT GGGTGGGTGG TTAAGACGTA 36240  
 GTGAGACCAAG ATGATTAAC TCAGCCGCGG TGCTGTGGGC TCACGCTGTG AACCCCAACA 36300  
 CTTTGGGAGG CGAGGCGGT AGGATCCCTC GAGGAATCGC CTACCCCTGT GGAGTGTAG 36360  
 GTTGCACTGA GTGACGCATA GTTGTGTCAC TGTGCTCCAG TCTGCGGAAA AGACAGATG 36420  
 AGGCCCTGCC ACAGGACGCG AGGCAGGCAG CAGGACGAGA AGCAACACTG TGTATTATGT 36480  
 TCTTCTCAGG GTAGGAACGA AAAATPAACG AATACAGCAC TTAATTAAAT TTTTTTTTGT 36540  
 CTTCTGGACG GTTGTCTACT TTGTGTGCC ACGCTGGAGT CAGTGGCAC CATCTCGGCT 36600  
 CACCGCAACC TCCACTCCCC CGGTTCAAGC GATTTCTCTG CCTCACCTC CTGAGTAGCT 36660  
 GGGATTTACG GAGGAGGCCA CCACACCCAG CTGATTTTGT ATTGTTAGTA GAGACGGCAT 36720  
 TTCTCCATGT GGTTCAGGCT GGTCTCGAAC TGGCGACCCC ATGTGATCTG CCGGCCCGCG 36780  
 CCTCCAAAG TGCTGGGGTG ACAGGCGTGA GCCATCTGTA CTGCGCGCTC ACCTTTTATTT 36840  
 ATTTATTTT TTAATTATTT TACTTTTTTT TAGTTTTCCA TTTTAACTTA TTTATTTAT 36900  
 TACATTTATT TATTATTTA TTATTTTACT TTTTCTGAGAC TTTTCTGAGC AGACTCTCGC 36960  
 TCTGCTGCCC AGGCTGGAGT GCAGCGGCGT GATCTCGGCT CACTGCAACG TCGCGCTCCC 37020  
 GGGTTACGCG CATCTCTCTG CTTCAGCCTC CCAAGTAGCT GGGACTACAG CGCCCGCTAG 37080  
 CGGTGCCCGG CTAACCTTTT GTATTTTGAG TAGAGATGGG GTTTCAGTGT GGTAGCCAGG 37140  
 ATGTTCTCGA TCTCTGACC CCGTGATCCG TCCACCTCGG CTTCCCAAAG TGCTGGGATG 37200  
 ACAGGCGTGA GCCACCGGCG CGGCGCTATT TATCTTTTTA TTAACCTTTGA GTCGAGTTTA 37260  
 TGAAACCACT TAGTTTTTGT AATTTTTTTT TTTTTTTTGA TTTTTTTAGA CAGAGTTTCA 37320  
 CCGTGTGCCC AAGGCTTGGA CCGAGGGGAT CACCGGCCCT CGGCCCTCCA AAGTGGCGGG 37380  
 GATGACAGGC GCGAGCCTAC CGCCCCCGGA CCCCCTTTCC CCCCCTTTCC CGCTTGTCTT 37440  
 CCGGACAGAC AGTTTTCAGG CAGAGCGTTT GGTGCGGTG CTTAAACTCA TCTTAAATAG 37500  
 AAATTTGGGA CGTCACTCTC TGGCTCTCAG GACTCTGAGC CAGGAGGTCC CCTGGTCTGT 37560  
 CTATCACAGG ACCGTACAGC TAAGGAGGAG AAAAATCGTA ACGTTCAAAG TCAAGTCAAT 37620  
 TGTGATACAG AAATACACCA ATTCACCAA AACACAGAAA ACACAGCTT AGAAATGGCC 37680  
 TTAGCCGCTG TGTCGCTGCC AGTGATTCTT TTGCGTTTGG ACCTTGACTG AGAGGATTCC 37740  
 CAGTGGGTGT CTGCTCTCTG GACGGAAGTT CCAGATGATC CGATGGGTGG GGGACTTAGG 37800  
 CTGCGTCCCC CAGAGAGGCC TGGTGCATTA GTTGTTGGGA TCGCTTTGGA GGGCGCGGTG 37860  
 ACCACTGTGT CTGTGGGAGT CTTCATCTTT CCCCACACC CTTCCCAGCG GGGATCCGAA 37920  
 TTACTTCCGG GCTGACACGC TCACTGGCAG GCGTGGGCGA TCACTTAGCG GTCACTGTTA 37980  
 CTTTGAARAC GAGAGGCTCA CAGAGGAAGG GAGCACCAGG CGCGCTAGCC ACAGCCTGGG 38040  
 GCACTGTGTT GCTTCCACAC CCCCCCGCCC CCACCTCCAA GTTCTCTCCCT CCGTTGTGG 38100  
 CTAGGAATCT CCCCCTTTGA CGACCCGGGT TGATTGACCT TTGATGACCT AAAAACGAC 38160  
 AAACAGATAA ATAAATAAAG TAACACAAA GTAACTAAT AAATAAATAA AGTCAATACA 38220  
 ACCATTAACA ATACAAATAG ATACGATACG ATAGGATGCG ATAGGATACG ATAGGATACA 38280  
 ATACATAGC ATACGATACA ATACAATACA ATACAATACA ATACAATACA ATACAATACA 38340  
 ATACATACA ATACATAGC CCGGGCGCGG TGGCTCATGC CTGTCACTC CCGCTTTTGG 38400  
 GATGCCGAGG TGGACGACT ACCTGAAGTC GGGAGTTTGA GACAAGCCCG AACCAACTAG 38460  
 AGAAATCCCG TCTCAATTGA AAATACAAA CTAGCCGGGC GCGGTGGCAC ATGCCTATA 38520

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TCCAGCTGC	TAGGAAGGCT	GAGGCAGGAG	AATCGCTTGA	ACCTGGGAAG	CGGAGGTTGC	38580
AGTGAGCCGA	GATTGCGCCA	TCGCACTCCA	GTCTGAGCAA	CAAGAGCGAA	ACTCCGTCTC	38640
AAAAATAAAT	ACATAATAA	ATACATACAT	ACATACATAC	ATACATACAT	ACATACATAC	38700
ATAAATAAAT	ATAAATAAAT	AAAAATAAAT	AAATAAATGG	GCCCTGCGCG	GTGGCTCAAG	38760
CTTGCTATCC	CCTCACTTTG	GGAGGCCAAG	GCCGGTGGAT	CAAGAGGCGCG	TCAGACCAAC	38820
AGGGCCAGTA	TGGTGAACCC	CCGTCTCTAC	TCACAATACA	CAACATTAGC	CGGGCGCTGT	38880
GCTGTGCTGT	ACTGTCTGTA	ATCCAGCTA	CTCGGAGGCG	CGAGCTGAGG	CAGGAGAATC	38940
GCTTGAACCT	GGGAGGCGGA	GTTTGCAGTG	AGCCGAGATC	GCCGCTACGT	AACTCCAGCT	39000
GGGCGACAGA	CGGAGACTCC	GTCTCCAAAA	AATGAAATG	AAAATGAAAC	GCAACAAAA	39060
AATTAATAAG	TGAGTTTCTG	GGGAAAAAGA	AGAAAAAGAA	AAAGAAAAAA	ACACAAAAAC	39120
AGACAACAAC	CACCGTGACA	TACACGTACG	CTTCTCGCTC	TTCGAGGCTC	CAACACAGTT	39180
AGGAATTATG	CGTGATTCTT	TTTTTTAACT	TCATTTTATG	TTATTTATGT	GATTTGATGT	39240
TCGAGACGGA	GTCTCGGAAG	CCCCGCCCTC	CTGGTTGCCC	AGACAACCCC	GGGAGACAGA	39300
CCCTGGCTGG	GCCCGATTGT	TCTTCTCCTT	GGTCAAGGGT	TTCCTTGCTC	TTCTTCGTGT	39360
CTTTAACCCG	CGTGGACTCT	TCGGCCTCGG	GTTTGACAGA	TGGCAGCTCC	ACTTTAGGCC	39420
TGTTTGTGTG	TGGGGACTTT	CCTGATTCTC	CCCAGATGTA	GTGAAAGCCG	GATGATTGCC	39480
TTCCTGCGCC	TGCTCTGCCC	TTCGCTTTTC	TTTCTTTCTT	TCCTTTCTTA	TTACTTTCTC	39540
TTTTTCTTCT	TCTTCTTCTT	CTTTTCTTTT	AGACAGAGTT	TCACTCTTGT	TGCCACAGCT	39600
AGAGGGCCAT	GCGCGCATCT	CGGCTCACCG	CACCTCCCGC	CTCCCAGGTT	CAAGCGATTC	39660
TCCTCGCTAA	GCTCTCTGAT	TGAGCTGGAT	TACAGGCATG	GCCCACCGTG	CGGCTGTATG	39720
TTTGTATCTT	TAGTAGAGAC	GSTGTTTTTC	CATGTTGGTC	AGGCTGGTCT	CCCACTGAGT	39780
ACCTCAGSTG	GTCCGCTCTC	CTTAGCCTCC	CAAGATGCTG	GGATGACAGG	CGTGCAACCG	39840
CGCCGACGCT	CTCCTCTCTC	CTCTCTCTCT	CTCGCTGCTG	TGCTTGCTGTG	CTTTCTGTGT	39900
TTCTTGCTTT	CGCGTTCTTT	TGCTTTCTTT	CTTCTCTCTG	TTTCTTTCAT	TTCTTGCTTC	39960
TGCTTGCTTT	TGCTTGCTTT	CTTCTCTCTG	TTCTTGCTTT	TTCTTGCTTT	TTCTTGCTTT	40020
TTTCTTTCTT	TGTTTCTTTT	CTTCTCTCTT	CTTCTCTCTT	CTTCTCTCTT	CTTCTCTCTT	40080
CTTGCTTTCC	TGTTTCTTTT	TTTCTCTCTT	TTTCTCTCTT	TTTCTCTCTT	TTTCTCTCTT	40140
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CTTGCTTTCC	TTTCTCTCTT	TTTCTCTCTT	TTTCTCTCTT	TTTCTCTCTT	TTTCTCTCTT	40260
CTTGCTTTCC	TTTCTCTCTT	TTTCTCTCTT	TTTCTCTCTT	TTTCTCTCTT	TTTCTCTCTT	40320
CTTGCTTTCC	TTTCTCTCTT	TTTCTCTCTT	TTTCTCTCTT	TTTCTCTCTT	TTTCTCTCTT	40380
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CTTGCTTTCC	TTTCTCTCTT	TTTCTCTCTT	TTTCTCTCTT	TTTCTCTCTT	TTTCTCTCTT	40620
CTTGCTTTCC	TTTCTCTCTT	TTTCTCTCTT	TTTCTCTCTT	TTTCTCTCTT	TTTCTCTCTT	40680
CTTGCTTTCC	TTTCTCTCTT	TTTCTCTCTT	TTTCTCTCTT	TTTCTCTCTT	TTTCTCTCTT	40740
CTTGCTTTCC	TTTCTCTCTT	TTTCTCTCTT	TTTCTCTCTT	TTTCTCTCTT	TTTCTCTCTT	40800
CTTGCTTTCC	TTTCTCTCTT	TTTCTCTCTT	TTTCTCTCTT	TTTCTCTCTT	TTTCTCTCTT	40860
CTTGCTTTCC	TTTCTCTCTT	TTTCTCTCTT	TTTCTCTCTT	TTTCTCTCTT	TTTCTCTCTT	40920
CTTGCTTTCC	TTTCTCTCTT	TTTCTCTCTT	TTTCTCTCTT	TTTCTCTCTT	TTTCTCTCTT	40980
CTTGCTTTCC	TTTCTCTCTT	TTTCTCTCTT	TTTCTCTCTT	TTTCTCTCTT	TTTCTCTCTT	41040
CTTGCTTTCC	TTTCTCTCTT	TTTCTCTCTT	TTTCTCTCTT	TTTCTCTCTT	TTTCTCTCTT	41100
CTTGCTTTCC	TTTCTCTCTT	TTTCTCTCTT	TTTCTCTCTT	TTTCTCTCTT	TTTCTCTCTT	41160
CTTGCTTTCC	TTTCTCTCTT	TTTCTCTCTT	TTTCTCTCTT	TTTCTCTCTT	TTTCTCTCTT	41220
CTTGCTTTCC	TTTCTCTCTT	TTTCTCTCTT	TTTCTCTCTT	TTTCTCTCTT	TTTCTCTCTT	41280
CTTGCTTTCC	TTTCTCTCTT	TTTCTCTCTT	TTTCTCTCTT	TTTCTCTCTT	TTTCTCTCTT	41340
CTTGCTTTCC	TTTCTCTCTT	TTTCTCTCTT	TTTCTCTCTT	TTTCTCTCTT	TTTCTCTCTT	41400
CTTGCTTTCC	TTTCTCTCTT	TTTCTCTCTT	TTTCTCTCTT	TTTCTCTCTT	TTTCTCTCTT	41460
CTTGCTTTCC	TTTCTCTCTT	TTTCTCTCTT	TTTCTCTCTT	TTTCTCTCTT	TTTCTCTCTT	41520
CTTGCTTTCC	TTTCTCTCTT	TTTCTCTCTT	TTTCTCTCTT	TTTCTCTCTT	TTTCTCTCTT	41580
CTTGCTTTCC	TTTCTCTCTT	TTTCTCTCTT	TTTCTCTCTT	TTTCTCTCTT	TTTCTCTCTT	41640
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CTTGCTTTCC	TTTCTCTCTT	TTTCTCTCTT	TTTCTCTCTT	TTTCTCTCTT	TTTCTCTCTT	41820
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CTTGCTTTCC	TTTCTCTCTT	TTTCTCTCTT	TTTCTCTCTT	TTTCTCTCTT	TTTCTCTCTT	41940
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CTTGCTTTCC	TTTCTCTCTT	TTTCTCTCTT	TTTCTCTCTT	TTTCTCTCTT	TTTCTCTCTT	42180
CTTGCTTTCC	TTTCTCTCTT	TTTCTCTCTT	TTTCTCTCTT	TTTCTCTCTT	TTTCTCTCTT	42240
CTTGCTTTCC	TTTCTCTCTT	TTTCTCTCTT	TTTCTCTCTT	TTTCTCTCTT	TTTCTCTCTT	42300
CTTGCTTTCC	TTTCTCTCTT	TTTCTCTCTT	TTTCTCTCTT	TTTCTCTCTT	TTTCTCTCTT	42360
CTTGCTTTCC	TTTCTCTCTT	TTTCTCTCTT	TTTCTCTCTT	TTTCTCTCTT	TTTCTCTCTT	42420

AGGCTGGGGA	CGCCCTTCCC	GGCCCGGTG	CGGTCCGCTC	ATCCTGGCCG	TCTGAGGCGG	42480
CGGCCGAATT	CGTTTCCGAG	ATCCCCGTGG	GGAGCCGGGG	ACCGTCCCGC	CCCCGTCCCC	42540
CGGGTGCCCG	GGAGCGGTTC	CCGGCCCGGG	CCGCGGTCCC	TCTGCCGCGA	TCCTTTCTGG	42600
CGAGTCCCCG	TGGCCAGTCG	GAGAGCGCTC	CCTGAGCCGG	TGCGGCCCGA	GAGGTGCGCG	42660
TGGCCGGCCT	TCGGTCCCTC	GTGTGTCCCG	GTCGTAGGAG	GGGCCGGCCG	AAAATGCTTC	42720
CGGCTCCCG	TCTGGAGACA	CGGGCCGGCC	CCTGCGTGTG	GCCAGGGCGG	CCGGGAGGGC	42780
TCCCCGGCCC	GGCGCTGTCC	CCGCGTGTGT	CCTTGGGTTG	ACCAGAGGGA	CCCCGGGGCG	42840
TCCGTGTGTG	GCTGCGATGG	TGGCGTTTTT	GGGGACAGGT	GTCCGTGTCC	GTGTGCGCGG	42900
TCGCTTGGG	CGGCGGCGTG	GTCCGTGACG	CGACTCTCCG	GCCCCGGGGG	AGGTATATCT	42960
TTGCTCTGCA	GTCCGCAATT	TTGGCCGGCC	GGGTTATAT			42999

## (2) INFORMATION FOR SEQ ID NO:18:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (iii) HYPOTHETICAL: NO

## (iv) ANTISENSE: NO

## (v) FRAGMENT TYPE:

## (vi) ORIGINAL SOURCE:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CTCCGCGCGG	GCCCCCGTGT	TCGCGTCTCC	CGTGGCGCGG	ACAATGCGGT	TGTGCGTCCA	60
CGTGTGCGTG	TCCGTGCAGT	GCCGTTGTGG	AGTGCCCTCG	TCTCCTCTCT	CTCCCGGCA	120
GCGTTCACAC	GTTTGGGGAC	CACGGGTGAC	CTCGCCCTCT	TCGGGCGCTG	ATCCG	175

## (2) INFORMATION FOR SEQ ID NO:19:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 755 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (iii) HYPOTHETICAL: NO

## (iv) ANTISENSE: NO

## (v) FRAGMENT TYPE:

## (vi) ORIGINAL SOURCE:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GGTCTGTTGG	GAATTGTTGA	CCTCGCTCTC	GGGTGCGGCC	TTTGGGGAAC	GGCGGGGTGG	60
GTCGTGCCCC	CGCCCGGACG	TGTTGTCGGG	CCCACTTCCC	GCTCGAGGGT	GGCGGTGGCG	120
CGCGCGTTGG	TAGTCTCCCC	TGTTGCGTCT	TCCCAGGCTC	TTGGGGGGGG	TGCGCTCGTT	180
TTCCGGGGCCG	CGGTGCTTGG	GCTTACGCAG	GCTTGGTTTG	GGACTGCCTC	AGGAGTCTGT	240
GGCGGTGTGA	TTCCCGCCGA	TTTTGCTCTG	CGTCTGCCTG	CTTTGCCTCG	GGTTTGCTTG	300
GTTCGTGTCT	CGGGAGCGGT	GGTTTTTTTT	TTTTTCGGGT	CCCCGGGAGA	GGGGTTTTTC	360
CGGGGAGCGT	TCCGCTCGCC	CCCTGCGGCC	GGTGGGTTTT	CGTTTCGGGC	TGTGTTCTGT	420
TCCCTTTCCT	CGTTTCGACG	TGGTTTCTCC	CCGCTCGGTC	GCGCCTCTCT	CCGCTCGGTC	480
GCCCCGCCCT	GCTGCCGGAC	CCCCCTTCT	GGGGGGGATG	CCCGGCGACG	CACGCTCCCG	540
GGCGGCCACT	GTGTTCCGGG	AGCTGCTCGG	CAGCGGGGTG	AGCCAGTTGG	AGGGGCGTGA	600
TGCCCCCGCG	GGCTCCCGTG	GCCGACGCGG	CGTGTTCCTT	GGGGGGGCTC	GTGCGTGGCG	660
GAAGGCTGCG	CACGTTGTGC	GTCCTTGCGA	GGGAAGAGGG	CTTTTTTTTT	TTAGGGGGTC	720
GTCTTCTGTC	GTCCCGTCGG	CGGTGGATCC	GGCCT			755

## (2) INFORMATION FOR SEQ ID NO:20:

## (i) SEQUENCE CHARACTERISTICS:



TTAGCTGAGT	TGTCCCGCGG	GGCCCGAAGC	GTTTACTTTG	AAAAAATTAG	AGTTGTTTCA	240
AAGCAGGCC	GAGCGCCTG	GATACCGCCA	GCTAGGAAT	AATGGAATAG	GACCGCGGTT	300
CCTATTGTT	TTGGTTTTG	GAAGTAGGCC	CATGATTAAG	GGAAACGGCC	GGGGGCGATT	360
CCTTATTGCG	CCCCCTA					378

## (2) INFORMATION FOR SEQ ID NO:23:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 719 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (iii) HYPOTHETICAL: NO

## (iv) ANTISENSE: NO

## (v) FRAGMENT TYPE:

## (vi) ORIGINAL SOURCE:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GGATCTTTCC	CGCTCCCCGT	TCCTCCGGCG	CCCTCCACCC	CGCGGTCTCC	CCCCCTCTTT	60
TCCCTCTCTC	GGAGGGGGGG	GAGGTGGGGG	CGCGTGGGGG	GGGTGCGGGG	TGGGTCGGGC	120
GGGGGACGCG	CCCCGGCGCG	CAAAAGGCGG	CGCGCGGGCG	CACCTCAACC	GTAGCGGTGC	180
GCGCGACGCG	GCTACGAGAC	GCGTGGGAAG	GCCCGACGGG	GAATGTGGCT	CGGGGGGGGC	240
GCGCGTCTC	AGGGCGCGCC	GAACCACTCT	ACCCCGAGTG	TTACAGCCCT	CCGGCCCGCG	300
TTTCGCGGAA	TCGCCGGGCG	GAGGGGAAGC	CGGATACCGG	TCGCCCGGCT	TTTCCCTCTC	360
CCCGCTCGCG	CTCCCGCGCG	GCGGTGGGGG	TGGGGGCGCG	GCGCGCCCTC	CCACGCCGCT	420
GGTTCTCTCT	TCCTCCGCTC	TCGCGCGGTT	TGGGGGGGGG	AGCCCGGTTG	GGGGCGGGCG	480
GGAAGTCTCT	CAGTGGCGCC	CGGGCGTCTG	CGCGCGCTCG	GGCCCGGGGG	GTCTCTCGGG	540
TCACGCCGAC	CCCGACGAAG	CCGAGCGCAC	GCGGTGCGCG	CGGATGTGCG	CTACCCACCC	600
GACCGCTCTT	GAAACACGGA	CCAAGGAGTC	TAACGCGTGC	GCGAGTCAGG	GGCTCGCACG	660
AAAGCCGCGG	TGGCGCAATG	AAGGTGAAGG	GCCCCGTCCG	GGGGCCCGAG	GTGGGATCC	719

## (2) INFORMATION FOR SEQ ID NO:24:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 685 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (iii) HYPOTHETICAL: NO

## (iv) ANTISENSE: NO

## (v) FRAGMENT TYPE:

## (vi) ORIGINAL SOURCE:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CGAGGCCCTCT	CCAGTCCGCC	GAGGGCGCAC	CACCGGCCCG	TCTCGCCCCG	CGCGTCGGGG	60
AGGTGGAGCA	CGAGCGTAGC	CGTTAGGACC	CGAAAGATGG	TGAAGTATGC	CTGGGCGAGG	120
CGAAGCCAGA	GGAAACTCTG	GTGGAGGTCT	GTAGCGGTCT	TGACGTGCAA	ATCGGTCTGT	180
CGACCTGGGT	ATAGGGGCGA	AAGACTAATC	GAACCATCTA	GTAGCTGGTT	CCCTCCGAAG	240
TTTCCCTCAG	GATAGCTGGC	GCTCTCGCAA	CCTTCGGAAG	CAGTTTATTC	CGGGTAAAGG	300
CGGAATGAT	TAGGAGGTCT	TGGGGCCGGA	AACGATCTCA	AACTATTCTC	CAAACTTTAA	360
ATGGGTAAAG	AAGCCCGGCT	CGCTGGCGTG	GAGCCGGGCG	TGGAATGCGA	GTGCTTAGTG	420
GGCCACTTTT	GGTAAGCAGA	ACTGGCGCTG	CGGGATGAAC	CGAACGCCGG	GTTAAGGCGC	480
CCGATGCGGA	CGCTCATCAG	ACCCACAGAA	AGGTGTTGGT	TGATATAGAC	AGCAGGAGCG	540
TGGCCATGGA	AGTCCGAATG	CGCTAAGGAG	TGTGTAAACA	CTCACTTGCC	GAATCAACTA	600
GCCCTGAAAA	TGGATGGCGC	TGGAGCGTCG	GGCCCATACC	CGGCCGTGCG	CGGCAGTGGG	660
AACGGGACGG	GACGGGAGCG	GCGCG				685

## (2) INFORMATION FOR SEQ ID NO:25:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (iii) HYPOTHETICAL: NO

## (iv) ANTISENSE: NO

## (v) FRAGMENT TYPE:

## (vi) ORIGINAL SOURCE:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GAGGAATTCC CCTATCCCTA ATCCAGATTG GTG

33

## (2) INFORMATION FOR SEQ ID NO:26:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (iii) HYPOTHETICAL: NO

## (iv) ANTISENSE: NO

## (v) FRAGMENT TYPE:

## (vi) ORIGINAL SOURCE:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

AAACTGCAGG CCGAGCCACC TCTCTCTGT GTTG

35

## (2) INFORMATION FOR SEQ ID NO:27:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (iii) HYPOTHETICAL: NO

## (iv) ANTISENSE: NO

## (v) FRAGMENT TYPE:

## (vi) ORIGINAL SOURCE:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

AGGAATTCAC AGAAGAGAGG TGGCTCGGCC TGC

33

## (2) INFORMATION FOR SEQ ID NO:28:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (iii) HYPOTHETICAL: NO

## (iv) ANTISENSE: NO

## (v) FRAGMENT TYPE:

## (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

AGCCTGCAGG AAGTCATACC TGGGAGGTG GCCC

34

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

AAACTGCAGG TTAATTAACC CTAACCCTAA CCCTAACCTT AACCTAACCT CTAACCCTAA  
CCCTAACCTT AACCCGGAT

60

80

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

TTGGGCCCTA GGCTTAAG

19

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GCCAGGGTTT TCCAGTCAC GACGT

25

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

GCTGCAAGGC GATTAAGTTG GGTAAC

26

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

TATGTTGTGT GGAATTGTGA GCGGAT

26

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GGGTTTAAAC AGATCTCTGC A

21